

09918568-080101

Sequence Listing

SEQ ID NO:1

LENGTH: 5

TYPE:amino acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:peptide

FLAGMENT TYPE:internal fragment

SEQUENCE DESCRIPTION:SEQ ID NO:1:

Thr Gly Leu Arg Asn

1

SEQ ID NO:2

LENGTH: 12

TYPE:amino acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:peptide

FLAGMENT TYPE:internal fragment

SEQUENCE DESCRIPTION:SEQ ID NO:2:

Gly Ile Thr Asn Lys Val Asn Ser Val Ile Glu Lys

1

5

10

SEQ ID NO:3

LENGTH: 5

TYPE:amino acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:peptide

FLAGMENT TYPE:internal fragment

SEQUENCE DESCRIPTION:SEQ ID NO:3:

Thr Gly Met Arg Asn

1

5

SEQ ID NO:4

LENGTH: 12

TYPE:amino acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:peptide

FLAGMENT TYPE:internal fragment

FEATURE:

LOCATION:9

NAME/KEY:Val or Leu

SEQUENCE DESCRIPTION:SEQ ID NO:5:

Gln Ile Asn Gly Lys Leu Asn Arg Xaa Ile Glu Lys

1

5

10

SEQ ID NO:5

LENGTH: 19

TYPE:nucleic acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:5:

AGCAAAAGCA GGGGATAAT 19

000105000-000101

SEQ ID NO:6

LENGTH: 21

TYPE:nucleic acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:6:

AGTAGAAACA AGGGTGT T 21

SEQ ID NO:7

LENGTH: 23

TYPE:nucleic acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:7:

TCTTTTCGAG TACTGTGTCA ACA 23

SEQ ID NO:8

LENGTH: 23

TYPE:nucleic acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:8:

GCCCCACTAC AATTGGGGAA ATG 23

SEQ ID NO:9

LENGTH: 24

TYPE:nucleic acid  
STRANDEDNESS:single  
TOPOLOGY:linear  
MOLECULE TYPE:Other nucleic acid (synthetic DNA)  
SEQUENCE DESCRIPTION:SEQ ID NO:9:  
TTTTACAGAA ATTTGCTATG GCTG 24

SEQ ID NO:10  
LENGTH: 24  
TYPE:nucleic acid  
STRANDEDNESS:single  
TOPOLOGY:linear  
MOLECULE TYPE:Other nucleic acid (synthetic DNA)  
SEQUENCE DESCRIPTION:SEQ ID NO:10:  
ACTCCCCTAT TGTGACTGGG TGTA 24

SEQ ID NO:11  
LENGTH: 22  
TYPE:nucleic acid  
STRANDEDNESS:single  
TOPOLOGY:linear  
MOLECULE TYPE:Other nucleic acid (synthetic DNA)  
SEQUENCE DESCRIPTION:SEQ ID NO:11:  
GGTTATCATC ATCAGAATGA AC 22

SEQ ID NO:12  
LENGTH: 24  
TYPE:nucleic acid  
STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:12:

AGTTCACCTT GTTTGTAATC CCGT 24

SEQ ID NO:13

LENGTH: 24

TYPE:nucleic acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:13:

CCATTTTTTA CTCTTCCAT GCAT 24

SEQ ID NO:14

LENGTH: 24

TYPE:nucleic acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:14:

ATCTACTCAA CTGTCGCCAG TTCA 24

SEQ ID NO:15

LENGTH: 23

TYPE:nucleic acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:15:

TTGTGTCGAC CTTCTCTGTG GAA 23

SEQ ID NO:16

LENGTH: 20

TYPE:nucleic acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:16:

TGTAGCATTG CCGGATGGCT 20

SEQ ID NO:17

LENGTH: 23

TYPE:nucleic acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:17:

ATTATCCGGT TGCCAAAGGA TCG 23

SEQ ID NO:18

LENGTH: 23

TYPE:nucleic acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:18:

GAGAGCACTG GTAATCTGTT GCA 23

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SEQ ID NO:19

LENGTH: 23

TYPE:nucleic acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:19:

CCATCAAATG CCTTTTGAGT GGA 23

SEQ ID NO:20

LENGTH: 23

TYPE:nucleic acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:20:

ACTAGAAGCT CAGCATTGTA TGT 23

SEQ ID NO:21

LENGTH: 24

TYPE:nucleic acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:21:

CATGCATTCA TCATCACATT TGTG 24

SEQ ID NO:22

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LENGTH: 23

TYPE:nucleic acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:22:

CATACTTGGG ATAATCATAC GTC 23

SEQ ID NO:23

LENGTH: 23

TYPE:nucleic acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:23:

GCCATTTATG CTACAGTAGC AGG 23

SEQ ID NO:24

LENGTH: 24

TYPE:nucleic acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:24:

GATCAGATTG AAGTGACTAA TGCT 24

SEQ ID NO:25

LENGTH: 24

TYPE:nucleic acid



STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:25:

GAATGCATCA CTCCAAATGG AAGC 24

SEQ ID NO:26

LENGTH: 23

TYPE:nucleic acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:26:

AGGTCCTGAA TTCTCCCTTC TAC 23

SEQ ID NO:27

LENGTH: 1754

TYPE:nucleic acid

STRANDEDNESS:double

TOPOLOGY:linear

MOLECULE TYPE:cdna to genomic RNA

ORIGINAL SOURCE:

ORGANISM:A/Suita/1/89

SEQUENCE DESCRIPTION:SEQ ID NO:27:

GGATAATAAA TACAACCAAA ATGAAAGCAA AACTACTAGT CCTGTTATGT GCATTTACAG	60
CTACAGATGC AGACACAATA TGTATAGGCT ACCATGCCAA CAACTCAACC GACACTGTTG	120
ACACAGTACT TGAGAAGAAC GTGACAGTGA CACACTCTGT CAACCTACTT GAGGACAGTC	180
ACAACGGAAA ACTATGTCGA CTAAAAGGAA TAGCCCCACT ACAATTGGGT AATTGCAGCA	240
TTGCCGGATG GATCTTAGGA AACCCAGAAT GCGAATCACT GTTTTCTAAG GAATCATGGT	300

CCTACATTGC	AGAAACACCA	AACTCCGAGA	ATGGAACATG	TTACCCAGGG	TATTTGCGCG	360
ACTATGAGGA	ACTGAGGGAG	CAATTGAGTT	CAGTATCATC	ATTCGAGAGA	TTCGAAATAT	420
TCCCCAAAGA	AAGCTCATGG	CCCAACCACA	CCGTAACCAA	AGGAGTAACG	GCATCATGCT	480
CCCATAATGG	GAAAAGCAGT	TTTTACAGAA	ATTTGCTATG	GCTGACGGGG	AAGAATGGCT	540
TGTACCCAAA	TCTGAGCAAG	TCCTATGTGA	ACAACAAAGA	GAAAGAAGTC	CTTGTAATAT	600
GGGGTGTTCA	TCACCCGTCT	AACATAGGGG	ACCAAAGGGC	CATCTATCAT	ACAGAAAATG	660
CTTATGTCTC	TGTAGTGTCT	TCACATTATA	GCAGGAGATT	CACCCCAGAA	ATAGCAAAAA	720
GACCCAAAGT	AAGAGGTCAA	GAAGGAAGAA	TTAACTACTA	CTGGACTCTG	CTGGAACCCG	780
GGGACACAAT	AATATTTGAG	GCAAAATGGAA	ATCTAATAGC	GCCATGGTAT	GCTTTTCGCAC	840
TGAGTAGAGG	CTTTGGGTCA	GGAATCATCA	CCTCAAACGC	ATCAATGGAT	GAATGTGACG	900
CGAAGTGTCA	AACACCCCAG	GGAGCTATAA	ACAGTAGTCT	TCCTTTCCAG	AATGTACACC	960
CAGTCACAAT	AGGAGAGTGT	CCAAAGTATG	TCAGGAGTAC	AAAATTAAGG	ATGGTTACAG	1020
GACTAAGGAA	CATCCCATCC	ATTCAATCCA	GAGGTTTGTG	TGGAGCCATT	GCCGGTTTCA	1080
TTGAAGGGGG	GTGGACTGGA	ATGATAGATG	GATGGTATGG	TTATCATCAT	CAGAATGAAC	1140
AAGGATCTGG	CTATGCTGCG	GATCAAAAAA	GCACACAAAA	TGCCATTAAC	GGAATTACAA	1200
ACAAGGTGAA	TTCTGTAATC	GAGAAAATGA	ACACTCAATT	CACAGCTGTG	GGCAAAGAAT	1260
TCAACAAATT	AGAAAGAAGG	ATGGAATACT	TAAATAAAAA	AGTTGATGAT	GGATTTCTGG	1320
ACATTTGGAC	ATATAATGCA	GAATTGTTGG	TTCTACTGGA	AAATGAAAGG	ACTTTGGATT	1380
TTCATGACTC	AAATGTGAAG	AATCTGTATG	AGAAAGTAAA	AAGCCAATTA	AAGAATAATG	1440
CCAAAGAAAT	AGGATACGGG	TGTTTTGAAT	TCTACCACAA	GTGTAACAAT	GAATGCATGG	1500
AAAGTGTGAA	AAATGGAACT	TATGACTATC	CAAAATATTC	CGAGGAATCA	AAGTTAAACA	1560
GGGAAAAAAT	TGATGGAGTG	AAATTGGAAT	CAATGGGAGT	CTATCAGATT	CTGGCGATCT	1620
ACTCAACTGT	CGCCAGTTCA	CTGGTGCTTT	TGGTCTCCCT	GGGGGCAATC	AGCTTCTGGA	1680
TGTGTTCTAA	TGGGTCTTTG	CAGTGTAGAA	TATGCATCTG	AGACCAGAAT	TTCAGAAATA	1740
TAAGAAAAAA	CACC					1754

SEQ ID NO:28

LENGTH: 1728

TYPE:nucleic acid

STRANDEDNESS:double

TOPOLOGY:linear

MOLECULE TYPE:cdna to genomic RNA

ORIGINAL SOURCE:

ORGANISM:A/Izumi/5/65

SEQUENCE DESCRIPTION:SEQ ID NO:28:

ATAGACAACC	AAAAGCATAA	CAATGGCCAT	CATCTATCTC	ATACTCCTGT	TCACAGCAGT	60
GAGGGGGGAC	CAGATATGCA	TTGGATACCA	TGCCAATAAT	TCCACAGAAA	AGGTCGACAC	120
AATTCTAGAG	CGGAATGTCA	CTGTGACTCA	TGCCAAGGAC	ATCCTTGAGA	AGACCCACAA	180
CGGAAAGCTA	TGCAAACTAA	ACGGAATCCC	TCCACTTGAA	CTAGGGGACT	GTAGCATTGC	240
CGGATGGCTC	CTTGGAATC	CAGAATGTGA	TAGGCTTCTA	AGGGTGCCAG	AATGGTCCTA	300
TATAATGGAG	AAAGAAAACC	CGAGATACAG	TTTATGTTAC	CCAGGCAACT	TCAATGACTA	360
TGAAGAATTG	AAACATCTCC	TCAGCAGCGT	AAAACATTTT	GAGAAAGTAA	AGATTCTGCC	420
CAAAGATAGA	TGGACACAGC	ATACAACAAC	TGGAGGTTCA	AAGGCCTGCG	CAGTGTGAGG	480
TAAACCATCA	TTCTTCAGGA	ACATGGTCTG	GCTGACAAAG	AAAGGACCAA	ATTATCCGGT	540
TGCCAAAGGA	TCGTACAACA	ATACGAGCGG	AGAGCAAATG	CTAATAATTT	GGGGAGTGCA	600
CCATCCTAAT	GATGAGGCAG	AACAAAGAGC	ATTGTACCAG	GAAGTGGGAA	CCTATGTTTC	660
CGCAAGCACA	TCAACATTGA	ACAAAAGGTC	AATCCCTGAA	ATAGCAGCAA	GGCCTAAAGT	720
GAATGGACTA	GGAAGTAGAA	TGGAATTCTC	TTGGACCCTC	TTGGATGTGT	GGGACACCAT	780
AAATTTTGAG	AGCACTGGTA	ATCTAGTTGC	ACCAGAGTAT	GGATTCAAAA	TATCGAAAAG	840
AGGTAGTTCA	GGGATCATGA	AGACAGAAGG	AACACTTGGG	AACTGTGAGA	CCAAATGCCA	900
AACTCCTTTG	GGAGCAATAA	ATACAACACT	ACCTTTTCAC	AATGTCCACC	CACTGACAAT	960
AGGTGAATGC	CCCAAATATG	TAAAATCGGA	GAAATTGGTC	TTAGCAACAG	GACTAAGGAA	1020
TGTTCCCCAG	ATTGAATCAA	GAGGATTGTT	TGGGGCAATA	GCTGGCTTTA	TAGAAGGAGG	1080
ATGGCAAGGA	ATGGTTGATG	GTTGGTATGG	ATACCATCAC	AGCAATGACC	AGGGATCAGG	1140
GTATGCAGCA	GACAAAGAAT	CCACTCAAAA	GGCATTGAT	GGAATCACCA	ACAAGGTAAA	1200
TTCTGTGATT	GAAAAGATGA	ACACCCAATT	TGAAGCTGTT	GGGAAAGAAT	TCAATAATTT	1260
AGAGAAAAGA	CTGGAGAACT	TGAACAAAAA	GATGGAAGAC	GGGTTTCTAG	ATGTGTGGAC	1320
ATACAATGCT	GAGCTTCTAG	TTCTGATGGA	AAATGAGAGG	ACACTTGACT	TCCATGATTC	1380

TAATGTCAAG AACCTGTATG ATAAAGTCAG AATGCAGCTG AGAGACAACG TCAAAGAACT	1440
AGGAAATGGA TGTTTTGAAT TTTATCACAA ATGTGACGAT GAATGCATGA ATAGTGTGAA	1500
AAACGGGACG TATGATTATC CCAAGTATGA AGAAGAATCT AAATAAATA GAAATGAAAT	1560
CAAAGGGGTA AAATTGAGCA GCATGGGGGT TTACCAAATT CTTGCCATTT ATGCTACAGT	1620
TGCAGGTTCT CTGTCACTGG CAATCATGAT GGCTGGGATC TCTTTCTGGA TGTGCTCCAA	1680
CGGGTCTCTG CAGTGCAGAA TCTGCATATG ATTGTAATTT ATTTTATA	1728

SEQ ID NO:29

LENGTH: 442

TYPE:nucleic acid

STRANDEDNESS:double

TOPOLOGY:linear

MOLECULE TYPE:cDNA to genomic RNA

ORIGINAL SOURCE:

ORGANISM:A/PR/8/34

SEQUENCE DESCRIPTION:SEQ ID NO:29:

CCTTTCCAGA ATATACACCC AGTCACAATA GGAGAGTGCC CAAAATACGT CAGGAGTGCC	60
AAATTGAGGA TGGTTACAGG ACTAAGGAAC ATCCCGTCCA TTCAATCCAG AGGTCTATTT	120
GGAGCCATTG CCGGTTTTAT TGAAGGGGGA TGGACTGGAA TGATAGATGG ATGGTATGGT	180
TATCATCATC AGAATGAACA GGGATCAGGC TATGCAGCGG ATCAAAAAAG CACACAAAAT	240
GCCATTAACG GGATTACAAA CAAGGTGAAC TCTGTTATCG AGAAAATGAA CACTCAATTC	300
ACAGCTGTGG GTAAAGAATT CAACAAATTA GAAAAAAGGA TGGAAAATTT AAATAAAAAA	360
GTTGATGATG GATTTCTGGA CATTTGGACA TATAATGCAG AATTGTTAGT TCTACTGGAA	420
AATGAAAGGA CTCTGGATTT CC	442

SEQ ID NO:30

LENGTH: 424

TYPE:nucleic acid

STRANDEDNESS:double

TOPOLOGY:linear

MOLECULE TYPE:cDNA to genomic RNA

ORIGINAL SOURCE:

ORGANISM:A/Bangkok/10/83

SEQUENCE DESCRIPTION:SEQ ID NO:30:

CCTTTCCAGA ATGTACACCC AGTCACAATA GGAGAGTGCC CAAAGTACGT CAGGAGTACA	60
AAATTAAGGA TGGTTACAGG ACTAAGGAAC ATCCCATCCA TTCAATCCAG AGGTTTGT	120
GGAGCCATTG CCGGTTTCAT TGAAGGGGGA TGGACTGGAA TGATAGATGG ATGGTATCGT	180
TATCATCATC AGAATGAACA AGGATCTGGC TATGCTGCGG ATCAAAAAAG CACACAAAAT	240
GCCATTAACG GGATTACAAA CAAGGTGAAC TCTGTAATCG AGAAAAATGAA CACTCAATTC	300
ACAGCTGTGG GTAAAGAATT CAACAAATTA GAAAAAGGA TGGAAAACTT AAATAAAAAA	360
GTTGATGATG GATTTCTGGA CATTTGGACA TATAATGCAG AATTGTTGGT TCTACTGGAA	420
AATG	424

SEQ ID NO:31

LENGTH: 424

TYPE:nucleic acid

STRANDEDNESS:double

TOPOLOGY:linear

MOLECULE TYPE:cDNA to genomic RNA

ORIGINAL SOURCE:

ORGANISM:A/Yamagata/120/86

SEQUENCE DESCRIPTION:SEQ ID NO:31:

CCTTTCCAGA ATGTACACCC AGTCACAATA GGAGAGTGCC CAAAGTATGT CAGGAGTACA	60
AAATTAAGGA TGGTTACAGG ACTAAGGAAC ATCCCATCCA TTCAATCCAG AGGTTTGT	120
GGAGCCATTG CCGGTTTCAT TGAAGGGGGG TGGACTGGAA TGATAGATGG ATGGTATGGT	180
TATCATCATC AGAATGAACA AGGATCTGGC TATGCTGCGG ATCAAAAAAG CACACAAAAT	240
GCCATTAACG GGATTACAAA CAAGGTGAAT TCTGTAATCG AGAAAAATGAA CACTCAATTC	300
ACAGCTGTGG GCAAAGAATT CAACAAATTA GAAAGAAGGA TGGAAAACTT AAATAAAAAA	360

GTTGATGATG GATTTCTGGA CATTTGGACA TATAATGCAG AATTGTTGGT CCTACTGGAA 420  
AATG 424

SEQ ID NO:32

LENGTH: 429

TYPE:nucleic acid

STRANDEDNESS:double

TOPOLOGY:linear

MOLECULE TYPE:cDNA to genomic RNA

ORIGINAL SOURCE:

ORGANISM:A/Osaka/930/88

SEQUENCE DESCRIPTION:SEQ ID NO:32:

CCTTTCCAGA ATGTACACCC AGTCACAATA GGAGAGTGCC CAAAGTATGT CAGGAGTACA 60  
AAATTAAGGA TGGTTACAGG ACTAAGGAAC ATCCCATCCA TTCAATCCAG AGGTTTGT TT 120  
GGAGCCATTG CCGGTTTCAT AGAAGGGGGG TGGACTGGAA TGATAGATGG ATGGTATGGT 180  
TATCATCATC AGAATGAACA AGGATCTGGC TATGCTGCGG ATCAAAAAAG CACACAAAAT 240  
GCCATTAACG GAATTACAAA CAAGGTGAAT TCTGTAATCG AGAAAATGAA CACTCAATTC 300  
ACAGCTGTGG GCAAAGAATT CAACAAATTA GAAAGAAGGA TGGAAAAC TT AAATAAAAAA 360  
GTTGATGATG GATTTCTGGA CATTTGGACA TATAATGCAG AATTGTTGGT TCTACTGGAA 420  
AATGAAAGG 429

SEQ ID NO:33

LENGTH: 400

TYPE:nucleic acid

STRANDEDNESS:double

TOPOLOGY:linear

MOLECULE TYPE:cDNA to genomic RNA

ORIGINAL SOURCE:

ORGANISM:A/Okuda/57

## SEQUENCE DESCRIPTION:SEQ ID NO:33:

GCAATAAATA CAACATTACC TTTTCACAAT GTCCACCCAC TGACAATAGG TGAGTGCCCC 60  
 AAATATGTAA AATCGGAGAA GTTGGTCTTA GCAACAGGAC TAAGGAATGT TCCCCAGATT 120  
 GAATCAAGAG GATTGTTTGG GGCAATAGCT GGTTTTATAG AAGGAGGATG GCAAGGAATG 180  
 GTTGACGGTT GGTATGGATA CCATCACAGC AATGACCAGG GATCAGGGTA TGCAGCAGAC 240  
 AAAGAATCCA CTCAAAAGGC ATTTGATGGA ATCACCAACA AGGTAAATTC TGTGATTGAA 300  
 AAGATAAACA CCCAATTTGA AGCTGTTGGG AAAGAATTCG GTAACCTAGA GAAAAGACTG 360  
 GAGAACTTGA ACAAAAAGAT GGAAGACGGG TTTCTAGATG 400

SEQ ID NO:34

LENGTH: 409

TYPE:nucleic acid

STRANDEDNESS:double

TOPOLOGY:linear

MOLECULE TYPE:cDNA to genomic RNA

ORIGINAL SOURCE:

ORGANISM:A/Adachi/2/57

## SEQUENCE DESCRIPTION:SEQ ID NO:34:

CGCCTTGGAG CAATAAATAC AACATTGCCT TTTACAATG TCCACCCACT GACAATAGGT 60  
 GAGTGCCCCA AATATGTAAA ATCGGAGAAG TTGGTCTTAG CAACAGGACT AAGGAATGTT 120  
 CCCCAGATTG AATCAAGAGG ATTGTTTGGG GCAATAGCTG GTTTTATAGA AGGAGGATGG 180  
 CAAGGAATGG TTGATGGTTG GTATGGATAC CATCACAGCA ATGACCAGGG ATCAGGGTAT 240  
 GCAGCAGACA AAGAATCCAC TCAAAAGGCA TTTGATGGAA TCACCAACAA GGTAAATTCT 300  
 GTGATTGAAA AGATGAACAC CCAATTTGAA GCTGTTGGGA AAGAATTCGG TAACTTAGAG 360  
 AGAAGACTGG AGAACTTGAA CAAAAAGATG GAAGACGGGT TTCTAGATG 409

SEQ ID NO:35

LENGTH: 410

TYPE:nucleic acid

STRANDEDNESS:double

TOPOLOGY:linear

MOLECULE TYPE:cDNA to genomic RNA

ORIGINAL SOURCE:

ORGANISM:A/Kumamoto/1/65

SEQUENCE DESCRIPTION:SEQ ID NO:36:

CTCCTTTGGA GCAATAAATA CAACATTACC TTTTCACAAT GTCCACCCAC TGACAATAGG 60  
TGAATGCCCC AAATATGTAA AATCGGAGAA ACTGGTCTTA GCAACAGGAG TAAGGAATGT 120  
TCCCCAGATT GAATCAAGAG GATTGTTTGG GGCAATAGCT GGCTTTGTAG AAGGAGGATG 180  
GCAAGGAATG ATTGATGGTT GGTATGGATA CCATCACAGC AATGATCAGG GATCAGGGTT 240  
TGCAGCAGAC AAAGAATCCA CTCAAAGGC ATTTGATGGA ATCACCAACA AGGTAAATTC 300  
TGTGATTGAA AAGATGAACA CCCAATTTGA AGCTGTTGGG AAAGAATTCA ATAATTTAGA 360  
GAAAAGACTG GAGAACTGA ACAAAGGAT GGAAGACGGG TTTCTAGATG 410

SEQ ID NO:36

LENGTH: 394

TYPE:nucleic acid

STRANDEDNESS:double

TOPOLOGY:linear

MOLECULE TYPE:cDNA to genomic RNA

ORIGINAL SOURCE:

ORGANISM:A/Kaizuka/2/65

SEQUENCE DESCRIPTION:SEQ ID NO:36:

AATACAACAC TACCTTTTCA CAATGTCCAC CCACTGACAA TAGGTGAATG CCCCAAATAT 60  
GTAAATCGG AGAAATTGGT CTTAGCAACA GACTAAGGA ATGTTCCCCA GATTGAATCA 120  
AGAGGATTGT TTGGGGCAAT AGCTGGCTTT ATAGAAGGAG GATGGCAAGG AATGGTTGAT 180  
GGTTGGTATG GATACCATCA CAGCAATGAC CAGGGATCAG GGTATGCAGC AGACAAAGAA 240  
TCCACTCAA AGGCATTTGA TGGAATCACC AACAAGGTAA ATTCTGTGAT TGAAAAGATG 300  
AACACCCAAT TTGAAGCTGT TGGGAAAGAA TTCAATAATT TAGAGAAAAG ACTGCAGAAC 360



TTGAACAAAA AGATGGAAGA CGGGTTTCTA GATG

394

SEQ ID NO:37

LENGTH: 329

TYPE:nucleic acid

STRANDEDNESS:double

TOPOLOGY:linear

MOLECULE TYPE:cDNA to genomic RNA

ORIGINAL SOURCE:

ORGANISM:A2/Aichi/2/68

SEQUENCE DESCRIPTION:SEQ ID NO:37:

ATGACAAGCC CTTTCAAAAC GTAAACAAGA TCACATATGG AGCATGCCCC AAGTATGTTA	60
AGCAAAACAC CCTGAAGTTG GCAACAGGGA TGC GGAATGT ACCAGAGAAA CAAACTAGAG	120
GCCTATTCGG CGCAATAGCA GGTTCATAG AAAATGGTTG GGAGGGAATG ATAGACGGTT	180
GGTACGGTTT CAGGCATCAA AATTCTGAGG GCACAGGACA AGCAGCAGAT CTTAAAAGCA	240
CTCAAGCAGC CATCGACCAA ATCAATGGGA AATTGAACAG GGTAATCGAG AAGACGAACG	300
AGAAATTCCA TCAAATCGAA AAGGAATTC	329

SEQ ID NO:38

LENGTH: 334

TYPE:nucleic acid

STRANDEDNESS:double

TOPOLOGY:linear

MOLECULE TYPE:cDNA to genomic RNA

ORIGINAL SOURCE:

ORGANISM:A/Fukuoka/C29/85

SEQUENCE DESCRIPTION:SEQ ID NO:38:

ATGACAAACC CTTTCAAAAT GTAAACAAGA TCACATATGG GGCATGTCCC AGGTATGTTA	60
AGCAAAACAC TCTGAAATTG GCAACAGGGA TGC GGAATGT ACCAGAGAAA CAAACTAGAG	120

GCATATTCGG CGCAATAGCA GGTTTCATAG AAAATGGTTG GGAGGGAATG GTAGACGGTT 180  
 GGTACGGTTT CAGGCATCAA AATTCTGAGG GCACAGGACA AGCAGCAGAT CTAAAAGCA 240  
 CTCAAGCAGC AATCGACCAA ATCAACGGGA AACTGAATAG GTTAATCGAG AAGACGAACG 300  
 AGAAATTCCA TCAAATCGAA AAGGAATTCT CAGA 334

SEQ ID NO:39

LENGTH: 329

TYPE:nucleic acid

STRANDEDNESS:double

TOPOLOGY:linear

MOLECULE TYPE:cDNA to genomic RNA

ORIGINAL SOURCE:

ORGANISM:A/Sichuan/2/87

SEQUENCE DESCRIPTION:SEQ ID NO:39:

ATGACAAACC CTTTCAAAT GTAAACAAGA TCACATATGG GGCATGTCCC AGATATGTTA 60  
 AGCAAAACAC TCTGAAATTG GCAACAGGGA TCGGGAATGT ACCAGAGAAA CAAACTAGAG 120  
 GCATATTCGG CGCAATAGCA GGTTTCATAG AAAATGGTTG GGAGGGAATG GTAGACGGCT 180  
 GGTACGGTTT CAGGCATCAA AATTCTGAGG GCACAGGACA AGCAGCAGAT CTAAAAGCA 240  
 CTCAAGCAGC AATCGACCAA ATCAACGGGA AACTGAATAG GTTAATCGAG AAGACGAACG 300  
 AGAAATTCCA TCAAACCGAA AAGGAATTC 329

SEQ ID NO:40

LENGTH: 334

TYPE:nucleic acid

STRANDEDNESS:double

TOPOLOGY:linear

MOLECULE TYPE:cDNA to genomic RNA

ORIGINAL SOURCE:

ORGANISM:A/Ibaraki/1/90

SEQUENCE DESCRIPTION:SEQ ID NO:40:

ATGACAAACC CTTTCAAAAT ATAAACAGGA TCACATATGG GGCATGTCCC AGATATGTTA	60
AGCAAAACAC TCTGAAATTG GCAACAGGGA TGC GGAATGT ACCAGAGAAA CAAACTAGAG	120
GCATATTCGG CGCAATCGCA GGTTCATAG AAAATGGTTG GGAGGGAATG GTAGACGGTT	180
GGTACGGTTT CAGGCATCAA AATTCTGAGG GCACAGGACA AGCAGCAGAT CTAAAAAGCA	240
CTCAAGCAGC AATCGACCAA ATCAACGGGA AACTGAATAG GTTAATCGAG AAGACGAACG	300
AGAAATTCCA TCAAATCGAA AAGGAATTCT CAGA	334

SEQ ID NO:41

LENGTH: 329

TYPE:nucleic acid

STRANDEDNESS:double

TOPOLOGY:linear

MOLECULE TYPE:cDNA to genomic RNA

ORIGINAL SOURCE:

ORGANISM:A/Suita/1/90

SEQUENCE DESCRIPTION:SEQ ID NO:41:

ATGACAAACC CTTTCAAAAT GTAAACAGGA TCACATATGG GGCATGTCCC AGATATGTTA	60
AGCAAAACAC TCTGAAATTG GCAACAGGGA TGC GGAATGT ACCAGAAAAA CAAACTAGGG	120
GCATATTCGG CGCAATCGCA GGTTCATAG AAAATGGTTG GGAGGGAATG GTAGACGGTT	180
GGTACGGTTT CAGGCATCAA AACTCTGAGG GCACAGGACA AGCAGCAGAT CTAAAAAGCA	240
CTCAAGCAGC AATCGACCAA ATCAACGGGA AACTGAATAG GTTAATCGAG AAGACGAACG	300
AGAAATTCCA TCAAACCGAA AAGGAATTC	329

SEQ ID NO:42

LENGTH: 30

TYPE:nucleic acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:42:

GATCTAGAAG CAAAAGCAGG GGTATACCA 30

SEQ ID NO:43

LENGTH: 30

TYPE:nucleic acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:43:

CGGCTAGCAA AAGCAGGGT TATACCATAG 30

SEQ ID NO:44

LENGTH: 29

TYPE:nucleic acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:44:

ACAGATCTAG TAGAAACAAG GGTGTTTTT 29

SEQ ID NO:45

LENGTH: 30

TYPE:nucleic acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:45:

CGGCTAGCAG AAACAAGGGT GTTTTTAATT 30

SEQ ID NO:46

LENGTH: 1783

TYPE:nucleic acid

STRANDEDNESS:double

TOPOLOGY:linear

MOLECULE TYPE:cDNA to genomic RNA

ORIGINAL SOURCE:

ORGANISM:A/Okuda/57

SEQUENCE DESCRIPTION:SEQ ID NO:46:

CGGCTAGCAA AAGCAGGGGT TATACCATAG AAAACCAAAA 40

GCAAAACA ATG GCC ATC ATT TAT CTC ATT CTC CTG TTC ACA GCA GTG AGA GGG 93

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly

-15

-10

-5

GAC CAG ATA TGC ATT GGA TAC CAT GCC AAT AAT TCC ACA GAG AAG 138

Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Lys

1

5

10

15

GTC GAC ACA ATT CTA GAG CGG AAC GTC ACT GTG ACT CAT GCC AAG 183

Val Asp Thr Ile Leu Glu Arg Asn Val Thr Val Thr His Ala Lys

20

25

30

GAC ATC CTT GAG AAG ACC CAT AAC GGA AAG TTA TGC AAA CTA AAC 228

Asp Ile Leu Glu Lys Thr His Asn Gly Lys Leu Cys Lys Leu Asn

35

40

45

GGA ATC CCT CCA CTT GAA CTA GGG GAC TGT AGC ATT GCC GGA TGG 273

Gly Ile Pro Pro Leu Glu Leu Gly Asp Cys Ser Ile Ala Gly Trp

50

55

60

CTC CTT GGA AAT CCA AAA TGT GAT AGG CTT CTA AGT GTG CCA GAA 318

Leu Leu Gly Asn Pro Lys Cys Asp Arg Leu Leu Ser Val Pro Glu

65	70	75	
CGG TCC TAT ATA TTG GAG AAA GAA AAC CCG AGA GAC GGT TTG TGT			363
Arg Ser Tyr Ile Leu Glu Lys Glu Asn Pro Arg Asp Gly Leu Cys			
80	85	90	
TAT CCA GGC AGC TTC AAT GAT TAT GAA GAA TTG AAA CAT CTC CTC			408
Tyr Pro Gly Ser Phe Asn Asp Tyr Glu Glu Leu Lys His Leu Leu			
95	100	105	
AGC AGC GTG AAA CAT TTC GAG AAA GTA AAG ATT CTG CCC AAA GAT			453
Ser Ser Val Lys His Phe Glu Lys Val Lys Ile Leu Pro Lys Asp			
110	115	120	
AGA TGG ACA CAG CAT ACA ACA ACT GGA GGT TCA CGG GCC TGC GCG			498
Arg Trp Thr Gln His Thr Thr Thr Gly Gly Ser Arg Ala Cys Ala			
125	130	135	
GTG TCT GGT AAT CCA TCA TTT TTC AGG AAC ATG GTC TGG CTG ACA			543
Val Ser Gly Asn Pro Ser Phe Phe Arg Asn Met Val Trp Leu Thr			
140	145	150	
AAG GAA GGA TCA GAT TAT CCG GTT GCC AAA GGA TCG TAC AAC AAT			588
Lys Glu Gly Ser Asp Tyr Pro Val Ala Lys Gly Ser Tyr Asn Asn			
155	160	165	
ACA AGC GGA GAA CAA ATG CTA ATA ATT TGG GGG GTG CAC CAT CCC			633
Thr Ser Gly Glu Gln Met Leu Ile Ile Trp Gly Val His His Pro			
170	175	180	
ATT GAT GAG ACA GAA CAA AGA ACA TTG TAC CAG AAT GTG GGA ACC			678
Ile Asp Glu Thr Glu Gln Arg Thr Leu Tyr Gln Asn Val Gly Thr			
185	190	195	
TAT GTT TCC GTA GGC ACA TCA ACA TTG AAC AAA AGG TCA ACC CCA			723
Tyr Val Ser Val Gly Thr Ser Thr Leu Asn Lys Arg Ser Thr Pro			
200	205	210	
GAA ATA GCA ACA AGG CCT AAA GTG AAT GGA CAA GGA GGT AGA ATG			768

Glu Ile Ala Thr Arg Pro Lys Val Asn Gly Gln Gly Gly Arg Met	
215	220 225
GAA TTC TCT TGG ACC CTC TTG GAT ATG TGG GAC ACC ATA AAT TTT	813
Glu Phe Ser Trp Thr Leu Leu Asp Met Trp Asp Thr Ile Asn Phe	
230	235 240
GAG AGT ACT GGT AAT CTA ATT GCA CCA GAG TAT GGA TTC AAA ATA	858
Glu Ser Thr Gly Asn Leu Ile Ala Pro Glu Tyr Gly Phe Lys Ile	
245	250 255
TCG AAA AGA GGT AGT TCA GGG ATC ATG AAA ACA GAA GGA ACA CTT	903
Ser Lys Arg Gly Ser Ser Gly Ile Met Lys Thr Glu Gly Thr Leu	
260	265 270
GAG AAC TGT GAG ACC AAA TGC CAA ACT CCT TTG GGA GCA ATA AAT	948
Glu Asn Cys Glu Thr Lys Cys Gln Thr Pro Leu Gly Ala Ile Asn	
275	280 285
ACA ACA TTA CCT TTT CAC AAT GTC CAC CCA CTG ACA ATA GGT GAG	993
Thr Thr Leu Pro Phe His Asn Val His Pro Leu Thr Ile Gly Glu	
290	295 300
TGC CCC AAA TAT GTA AAA TCG GAG AAG TTG GTC TTA GCA ACA GGA	1038
Cys Pro Lys Tyr Val Lys Ser Glu Lys Leu Val Leu Ala Thr Gly	
305	310 315
CTA AGG AAT GTT CCC CAG ATT GAA TCA AGA GGA TTG TTT GGG GCA	1083
Leu Arg Asn Val Pro Gln Ile Glu Ser Arg Gly Leu Phe Gly Ala	
320	325 330
ATA GCT GGT TTT ATA GAA GGA GGA TGG CAA GGA ATG GTT GAC GGT	1128
Ile Ala Gly Phe Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly	
335	330 345
TGG TAT GGA TAC CAT CAC AGC AAT GAC CAG GGA TCA GGG TAT GCA	1173
Trp Tyr Gly Tyr His His Ser Asn Asp Gln Gly Ser Gly Tyr Ala	
350	355 360

GCA GAC AAA GAA TCC ACT CAA AAG GCA TTT GAT GGA ATC ACC AAC	1218
Ala Asp Lys Glu Ser Thr Gln Lys Ala Phe Asp Gly Ile Thr Asn	
365 370 375	
AAG GTA AAT TCT GTG ATT GAA AAG ATA AAC ACC CAA TTT GAA GCT	1263
Lys Val Asn Ser Val Ile Glu Lys Ile Asn Thr Gln Phe Glu Ala	
380 385 390	
GTT GGG AAA GAA TTC GGT AAC TTA GAG AAA AGA CTG GAG AAC TTG	1308
Val Gly Lys Glu Phe Gly Asn Leu Glu Lys Arg Leu Glu Asn Leu	
395 400 405	
AAC AAA AAG ATG GAA GAC GGG TTT CTA GAT GTG TGG ACA TAC AAT	1353
Asn Lys Lys Met Glu Asp Gly Phe Leu Asp Val Trp Thr Tyr Asn	
410 415 420	
GCT GAG CTT TTA GTT CTG ATG GAA AAT GAG AGG ACA CTT GAC TTT	1398
Ala Glu Leu Leu Val Leu Met Glu Asn Glu Arg Thr Leu Asp Phe	
425 430 435	
CAT GAT TCT AAT GTC AAG AAT CTG TAT AGT AAA GTC AGA ATG CAG	1443
His Asp Ser Asn Val Lys Asn Leu Tyr Ser Lys Val Arg Met Gln	
440 445 450	
CTG AGA GAC AAC GTC AAA GAA CTA GGA AAT GGA TGT TTT GAA TTT	1488
Leu Arg Asp Asn Val Lys Glu Leu Gly Asn Gly Cys Phe Glu Phe	
455 460 465	
TAT CAC AAA TGT GAT GAT GAA TGC ATG AAT AGT GTG AAA AAC GGG	1533
Tyr His Lys Cys Asp Asp Glu Cys Met Asn Ser Val Lys Asn Gly	
470 475 480	
ACA TAT GAT TAT CCC AAG TAT GAA GAA GAG TCT AAA CTA AAT AGA	1578
Thr Tyr Asp Tyr Pro Lys Tyr Glu Glu Glu Ser Lys Leu Asn Arg	
495 500 505	
AAT GAA ATC AAA GGG GTA AAA TTG AGC AGC ATG GGG GTT TAT CAA	1623
Asn Glu Ile Lys Gly Val Lys Leu Ser Ser Met Gly Val Tyr Gln	



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510	515	520	
ATC CTT GCC ATT TAT GCT ACA GTA GCA GGT TCT ATG TCA CTG GCA			1668
Ile Leu Ala Ile Tyr Ala Thr Val Ala Gly Ser Met Ser Leu Ala			
525	530	535	
ATC ATG ATG GCT GGG ATC TCT TTC TGG GTG TGC TCC AAC GGG TCT			1713
Ile Met Met Ala Gly Ile Ser Phe Trp Val Cys Ser Asn Gly Ser			
540	545	550	
CTG CAG TGC AGG ATC TGC ATA TGATTATAAG TCATTTTATA ATTAAAAACA			1764
Leu Gln Cys Arg Ile Cys Ile			
555			
CCCTTGTTTC TGCTAGCCG			1783

SEQ ID NO:47

LENGTH: 25

TYPE:nucleic acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:47:

TCCGTTTAGT TTGCATAACT TTCCG 25

SEQ ID NO:48

LENGTH: 26

TYPE:nucleic acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:Other nucleic acid (synthetic DNA)

SEQUENCE DESCRIPTION:SEQ ID NO:48:

TCCGGGATCA TGAAAAACAGA AGGAAC 26

SEQ ID NO:49

LENGTH: 1135

TYPE:nucleic acid

STRANDEDNESS:double

TOPOLOGY:linear

MOLECULE TYPE:cdna to genomic RNA

ORIGINAL SOURCE:

ORGANISM:A/Okuda/57

SEQUENCE DESCRIPTION:SEQ ID NO:49:

CTAGCAAAAG CAGGGGTTAT ACCATAGAAA ACCAAAAGCA AAACAATGGC CATCATTTAT	60
CTCATTCTCC TGTTCACAGC AGTGAGAGGG GACCAGATAT GCATTGGATA CCATGCCAAT	120
AATTCCACAG AGAAGGTCGA CACAATTCTA GAGCGGAACG TCACTGTGAC TCATGCCAAG	180
GACATCCTTG AGAAGACCCA TAACGGAAAG TTATGCAAAC TAAACGGATC CGGGATCATG	240
AAAACAGAAG GAACACTTGA GAACTGTGAG ACCAAATGCC AAACCTCCTTT GGGAGCAATA	300
AATACAACAT TACCTTTTCA CAATGTCCAC CCACTGACAA TAGGTGAGTG CCCCAAATAT	360
GTAAAATCGG AGAAGTTGGT CTTAGCAACA GGAATAAGGA ATGTTCCCCA GATTGAATCA	420
AGAGGATTGT TTGGGGCAAT AGCTGGTTTT ATAGAAGGAG GATGGCAAGG AATGGTTGAC	480
GGTTGGTATG GATACCATCA CAGCAATGAC CAGGGATCAG GGTATGCAGC AGACAAAGAA	540
TCCACTCAAA AGGCATTTGA TGAATCACC AACAAGGTAA ATTCTGTGAT TGAAAAGATA	600
AACACCCAAT TTGAAGCTGT TGGGAAAGAA TTCGGTAACT TAGAGAAAAG ACTGGAGAAC	660
TTGAACAAAA AGATGGAAGA CGGGTTTCTA GATGTGTGGA CATACAATGC TGAGCTTTTA	720
GTTCTGATGG AAAATGAGAG GACACTTGAC TTTTCATGATT CTAATGTCAA GAATCTGTAT	780
AGTAAAGTCA GAATGCAGCT GAGAGACAAC GTCAAAGAAC TAGGAAATGG ATGTTTTGAA	840
TTTTATCACA AATGTGATGA TGAATGCATG AATAGTGTGA AAAACGGGAC ATATGATTAT	900
CCCAAGTATG AAGAAGAGTC TAAACTAAAT AGAAATGAAA TCAAAGGGGT AAAATTGAGC	960
AGCATGGGGG TTTATCAAAT CCTTGCCATT TATGCTACAG TAGCAGGTTT TATGTCACTG	1020
GCAATCATGA TGGCTGGGAT CTCTTTCTGG GTGTGCTCCA ACGGGTCTCT GCAGTGCAGG	1080
ATCTGCATAT GATTATAAGT CATTTTATAA TTA AAAACAC CCTTGTTTCT GCTAG	1135

SEQ ID NO:50

LENGTH: 348

TYPE:amino acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:peptide

SEQUENCE DESCRIPTION:SEQ ID NO:50:

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly  
-15 -10 -5

Asp Gln Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Lys  
1 5 10 15

Val Asp Thr Ile Leu Glu Arg Asn Val Thr Val Thr His Ala Lys  
20 25 30

Asp Ile Leu Glu Lys Thr His Asn Gly Lys Leu Cys Lys Leu Asn  
35 40 45

Gly Ser Gly Ile Met Lys Thr Glu Gly Thr Leu Glu Asn Cys Glu  
50 55 60

Thr Lys Cys Gln Thr Pro Leu Gly Ala Ile Asn Thr Thr Leu Pro  
65 70 75

Phe His Asn Val His Pro Leu Thr Ile Gly Glu Cys Pro Lys Tyr  
80 85 90

Val Lys Ser Glu Lys Leu Val Leu Ala Thr Gly Leu Arg Asn Val  
95 100 105

Pro Gln Ile Glu Ser Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe  
110 115 120

Ile Glu Gly Gly Trp Gln Gly Met Val Asp Gly Trp Tyr Gly Tyr  
125 130 135

His His Ser Asn Asp Gln Gly Ser Gly Tyr Ala Ala Asp Lys Glu

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140	145	150
Ser Thr Gln Lys Ala Phe Asp Gly Ile Thr Asn Lys Val Asn Ser		
155	160	165
Val Ile Glu Lys Ile Asn Thr Gln Phe Glu Ala Val Gly Lys Glu		
170	175	180
Phe Gly Asn Leu Glu Lys Arg Leu Glu Asn Leu Asn Lys Lys Met		
185	190	195
Glu Asp Gly Phe Leu Asp Val Trp Thr Tyr Asn Ala Glu Leu Leu		
200	205	210
Val Leu Met Glu Asn Glu Arg Thr Leu Asp Phe His Asp Ser Asn		
215	220	225
Val Lys Asn Leu Tyr Ser Lys Val Arg Met Gln Leu Arg Asp Asn		
230	235	240
Val Lys Glu Leu Gly Asn Gly Cys Phe Glu Phe Tyr His Lys Cys		
245	250	255
Asp Asp Glu Cys Met Asn Ser Val Lys Asn Gly Thr Tyr Asp Tyr		
260	265	270
Pro Lys Tyr Glu Glu Glu Ser Lys Leu Asn Arg Asn Glu Ile Lys		
275	280	285
Gly Val Lys Leu Ser Ser Met Gly Val Tyr Gln Ile Leu Ala Ile		
290	295	300
Tyr Ala Thr Val Ala Gly Ser Met Ser Leu Ala Ile Met Met Ala		
305	310	315
Gly Ile Ser Phe Trp Val Cys Ser Asn Gly Ser Leu Gln Cys Arg		
320	325	330
Ile Cys Ile		

SEQ ID NO:51

LENGTH: 30

TYPE:nucleic acid  
STRANDEDNESS:single  
TOPOLOGY:linear  
MOLECULE TYPE:Other nucleic acid (synthetic DNA)  
SEQUENCE DESCRIPTION:SEQ ID NO:51:  
GATCTAGAAG CAAAGCAGGG GATAATTCTA 30

SEQ ID NO:52  
LENGTH: 29  
TYPE:nucleic acid  
STRANDEDNESS:single  
TOPOLOGY:linear  
MOLECULE TYPE:Other nucleic acid (synthetic DNA)  
SEQUENCE DESCRIPTION:SEQ ID NO:52:  
ACAGATCTAG TAGAAACAAG GGTGTTTTT 29

SEQ ID NO:53  
LENGTH: 30  
TYPE:nucleic acid  
STRANDEDNESS:single  
TOPOLOGY:linear  
MOLECULE TYPE:Other nucleic acid (synthetic DNA)  
SEQUENCE DESCRIPTION:SEQ ID NO:53:  
CGGCTAGCAG AAACAAGGGT GTTTTAAATT 30

SEQ ID NO:54  
LENGTH: 1778  
TYPE:nucleic acid  
STRANDEDNESS:double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to genomic RNA

ORIGINAL SOURCE:

ORGANISM: A2/Aichi/2/68

SEQUENCE DESCRIPTION: SEQ ID NO: 54:

GATCTAGAAG CAAAGCAGGG GATAATTCTA 30  
TTAATC ATG AAG ACC ATC ATT GCT TTG AGC TAC ATT TTC TGT CTG GCT CTC 81  
Met Lys Thr Ile Ile Ala Leu Ser Tyr Ile Phe Cys Leu Ala Leu  
-15 -10 -5  
GGC CAA GAC CTT CCA GGA AAT GAC AAC AGC ACA GCA ACG CTG TGC 127  
Gly Gln Asp Leu Pro Gly Asn Asp Asn Ser Thr Ala Thr Leu Cys  
1 5 10  
CTG GGA CAT CAT GCG GTG CCA AAC GGA ACA CTA GTG AAA ACA ATC 172  
Leu Gly His His Ala Val Pro Asn Gly Thr Leu Val Lys Thr Ile  
15 20 25  
ACA GAT GAT CAG ATT GAA GTG ACT AAT GCT ACT GAG CTA GTT CAG 217  
Thr Asp Asp Gln Ile Glu Val Thr Asn Ala Thr Glu Leu Val Gln  
30 35 40  
AGC TCC TCA ACG GGG AAA ATA TGC AAC AAT CCT CAT CGA ATC CTT 262  
Ser Ser Ser Thr Gly Lys Ile Cys Asn Asn Pro His Arg Ile Leu  
45 50 55  
GAT GGA ATA GAC TGC ACA CTG ATA GAT GCT CTA TTG GGG GAC CCT 307  
Asp Gly Ile Asp Cys Thr Leu Ile Asp Ala Leu Leu Gly Asp Pro  
60 65 70  
CAT TGT GAT GTT TTT CAA AAT GAG ACA TGG GAC CTT TTC GTT GAA 352  
His Cys Asp Val Phe Gln Asn Glu Thr Trp Asp Leu Phe Val Glu  
75 80 85  
CGC AGC AAA GCT TTC AGC AAC TGT TAC CCT TAT GAT GTG CCA GAT 397  
Arg Ser Lys Ala Phe Ser Asn Cys Tyr Pro Tyr Asp Val Pro Asp

90	95	100	
TAT GCC TCC CTT AGG TCA CTA GTT GCC TCG TCA GGC ACT CTG GAG			442
Tyr Ala Ser Leu Arg Ser Leu Val Ala Ser Ser Gly Thr Leu Glu			
105	110	115	
TTT ATC ACT GAG GGT TTC ACT TGG ACT GGG GTC ACT CAG AAT GGG			487
Phe Ile Thr Glu Gly Phe Thr Trp Thr Gly Val Thr Gln Asn Gly			
120	125	130	
GGA AGC AAT GCT TGC AAA AGG GGA CCT GGT AGC GGT TTT TTC AGT			532
Gly Ser Asn Ala Cys Lys Arg Gly Pro Gly Ser Gly Phe Phe Ser			
135	140	145	
AGA CTG AAC TGG TTG ACC AAA TCA GGA AGC ACA TAT CCA GTG CTG			577
Arg Leu Asn Trp Leu Thr Lys Ser Gly Ser Thr Tyr Pro Val Leu			
150	155	160	
AAC GTG ACT ATG CCA AAC AAT GAC AAT TTT GAC AAA CTA TAC ATT			622
Asn Val Thr Met Pro Asn Asn Asp Asn Phe Asp Lys Leu Tyr Ile			
165	170	175	
TGG GGG ATT CAC CAC CCG AGC ACG AAC CAA GAA CAA ACC AGC CTG			667
Trp Gly Ile His His Pro Ser Thr Asn Gln Glu Gln Thr Ser Leu			
180	185	190	
TAT GTT CAA GCA TCA GGG AGA GTC ACA GTC TCT ACC AGG AGA AGC			712
Tyr Val Gln Ala Ser Gly Arg Val Thr Val Ser Thr Arg Arg Ser			
195	200	205	
CAG CAA ACT ATA ATC CCG AAT ATC GGG TCC AGA CCC TGG GTA AGG			757
Gln Gln Thr Ile Ile Pro Asn Ile Gly Ser Arg Pro Trp Val Arg			
210	215	220	
GGT CTG TCT AGT AGA ATA AGC ATC TAT TGG ACA ATA GTT AAG CCG			802
Gly Leu Ser Ser Arg Ile Ser Ile Tyr Trp Thr Ile Val Lys Pro			
225	230	235	
GGA GAC GTA CTG GTA ATT AAT AGT AAT GGG AAC CTA ATC GCT CCT			847

Gly Asp Val Leu Val Ile Asn Ser Asn Gly Asn Leu Ile Ala Pro	
240	245 250
CGG GGT TAT TTC AAA ATG CGC ACT GGG AAA AGC TCA ATA ATG AGG	892
Arg Gly Tyr Phe Lys Met Arg Thr Gly Lys Ser Ser Ile Met Arg	
255	260 265
TCA GAT GCA CCT ATT GAT ACC TGT ATT TCT GAA TGC ATC ACT CCA	937
Ser Asp Ala Pro Ile Asp Thr Cys Ile Ser Glu Cys Ile Thr Pro	
270	275 280
AAT GGA AGC ATT CCC AAT GAC AAG CCC TTT CAA AAC GTA AAC AAG	982
Asn Gly Ser Ile Pro Asn Asp Lys Pro Phe Gln Asn Val Asn Lys	
285	290 295
ATC ACA TAT GGA GCA TGC CCC AAG TAT GTT AAG CAA AAC ACC CTG	1027
Ile Thr Tyr Gly Ala Cys Pro Lys Tyr Val Lys Gln Asn Thr Leu	
300	305 310
AAG TTG GCA ACA GGG ATG CGG AAT GTA CCA GAG AAA CAA ACT AGA	1072
Lys Leu Ala Thr Gly Met Arg Asn Val Pro Glu Lys Gln Thr Arg	
315	320 325
GGC CTA TTC GGC GCA ATA GCA GGT TTC ATA GAA AAT GGT TGG GAG	1117
Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Glu	
330	335 340
GGA ATG ATA GAC GGT TGG TAC GGT TTC AGG CAT CAA AAT TCT GAG	1162
Gly Met Ile Asp Gly Trp Tyr Gly Phe Arg His Gln Asn Ser Glu	
345	350 355
GGC ACA GGA CAA GCA GCA GAT CTT AAA AGC ACT CAA GCA GCC ATC	1207
Gly Thr Gly Gln Ala Ala Asp Leu Lys Ser Thr Gln Ala Ala Ile	
360	365 370
GAC CAA ATC AAT GGG AAA TTG AAC AGG GTA ATC GAG AAG ACG AAC	1252
Asp Gln Ile Asn Gly Lys Leu Asn Arg Val Ile Glu Lys Thr Asn	
375	380 385



GAG AAA TTC CAT CAA ATC GAA AAG GAA TTC TCA GAA GTA GAA GGG	1297
Glu Lys Phe His Gln Ile Glu Lys Glu Phe Ser Glu Val Glu Gly	
390 395 400	
AGA ATT CAG GAC CTC GAG AAA TAC GTT GAA GAC ACT AAA ATA GAT	1342
Arg Ile Gln Asp Leu Glu Lys Tyr Val Glu Asp Thr Lys Ile Asp	
405 410 415	
CTC TGG TCT TAC AAT GCG GAG CTT CTT GTC GCT CTG GAG AAT CAA	1387
Leu Trp Ser Tyr Asn Ala Glu Leu Leu Val Ala Leu Glu Asn Gln	
420 425 430	
CAT ACA ATT GAC CTG ACT GAC TCG GAA ATG AAC AAG CTG TTT GAA	1432
His Thr Ile Asp Leu Thr Asp Ser Glu Met Asn Lys Leu Phe Glu	
435 440 445	
AAA ACA AGG AGG CAA CTG AGG GAA AAT GCT GAA GAG ATG GGC AAT	1477
Lys Thr Arg Arg Gln Leu Arg Glu Asn Ala Glu Glu Met Gly Asn	
450 455 460	
GGT TGC TTC AAA ATA TAC CAC AAA TGT GAC AAC GCT TGC ATA GAG	1522
Gly Cys Phe Lys Ile Tyr His Lys Cys Asp Asn Ala Cys Ile Glu	
465 470 475	
TCA ATC AGA AAT GGT ACT TAT GAC CAT GAT GTA TAC AGA GAC GAA	1567
Ser Ile Arg Asn Gly Thr Tyr Asp His Asp Val Tyr Arg Asp Glu	
480 485 490	
GCA TTA AAC AAC CGG TTT CAG ATC AAA GGT GTT GAA CTG AAG TCT	1612
Ala Leu Asn Asn Arg Phe Gln Ile Lys Gly Val Glu Leu Lys Ser	
495 500 505	
GGA TAC AAA GAC TGG ATC CTG TGG ATT TCC TTT GCC ATA TCA TGC	1657
Gly Tyr Lys Asp Trp Ile Leu Trp Ile Ser Phe Ala Ile Ser Cys	
510 515 520	
TTT TTG CTT TGT GTT GTT TTG CTG GGG TTC ATC ATG TGG GCC TGC	1702
Phe Leu Leu Cys Val Val Leu Leu Gly Phe Ile Met Trp Ala Cys	

525                      530                      535  
 CAG AGA GGC AAC ATT AGG TGC AAC ATT TGC ATT TGAGTGTATT AGTAATTAAA 1755  
 Gln Arg Gly Asn Ile Arg Cys Asn Ile Cys Ile  
 40                      545                      550  
 AACACCCTTG TTTCTGCTAG CCG 1778

SEQ ID NO:55  
 LENGTH: 20  
 TYPE:nucleic acid  
 STRANDEDNESS:single  
 TOPOLOGY:linear  
 MOLECULE TYPE:Other nucleic acid (synthetic DNA)  
 SEQUENCE DESCRIPTION:SEQ ID NO:55:  
 ATTGTTGCAT ATTTTCCCCG 20

SEQ ID NO:56  
 LENGTH: 20  
 TYPE:nucleic acid  
 STRANDEDNESS:single  
 TOPOLOGY:linear  
 MOLECULE TYPE:Other nucleic acid (synthetic DNA)  
 SEQUENCE DESCRIPTION:SEQ ID NO:56:  
 ATTGATACCT GTATTTCTGA 20

SEQ ID NO:57  
 LENGTH: 1110  
 TYPE:STRANDEDNESS:double  
 TOPOLOGY:linear  
 MOLECULE TYPE:cDNA to genomic RNA

ORIGINAL SOURCE:

ORGANISM:A2/Aichi/2/68

SEQUENCE DESCRIPTION:SEQ ID NO:57:

CTAGAAGCAA AGCAGGGGAT AATTCTATTA ATCATGAAGA CCATCATTGC TTTGAGCTAC	60
ATTTTCTGTC TGGCTCTCGG CCAAGACCTT CCAGGAAATG ACAACAGCAC AGCAACGCTG	120
TGCCTGGGAC ATCATGCGGT GCCAAACGGA ACACTAGTGA AAACAATCAC AGATGATCAG	180
ATTGAAGTGA CTAATGCTAC TGAGCTAGTT CAGAGCTCCT CAACGGGGAA AATATGCAAC	240
AATATTGATA CCTGTATTTT TGAATGCATC ACTCCAAATG GAAGCATTCC CAATGACAAG	300
CCCTTTCAAA ACGTAAACAA GATCACATAT GGAGCATGCC CCAAGTATGT TAAGCAAAAC	360
ACCTTGAAGT TGGCAACAGG GATGCGGAAT GTACCAGAGA AACAACTAG AGGCCTATTC	420
GGCGCAATAG CAGGTTTCAT AGAAAATGGT TGGGAGGGAA TGATAGACGG TTGGTACGGT	480
TTCAGGCATC AAAATTCTGA GGGCACAGGA CAAGCAGCAG ATCTTAAAAG CACTCAAGCA	540
GCCATCGACC AAATCAATGG GAAATTGAAC AGGGTAATCG AGAAGACGAA CGAGAAATTC	600
CATCAAATCG AAAAGGAATT CTCAGAAGTA GAAGGGAGAA TTCAGGACCT CGAGAAATAC	660
GTTGAAGACA CTAATAATAGA TCTCTGGTCT TACAATGCGG AGCTTCTTGT CGCTCTGGAG	720
AATCAACATA CAATTGACCT GACTGACTCG GAAATGAACA AGCTGTTTGA AAAAACAAGG	780
AGGCAACTGA GGGAAAATGC TGAAGAGATG GGCAATGGTT GCTTCAAAAT ATACCAACAA	840
TGTGACAACG CTTGCATAGA GTCAATCAGA AATGGTACTT ATGACCATGA TGTATACAGA	900
GACGAAGCAT TAAACAACCG GTTTCAGATC AAAGGTGTTG AACTGAAGTC TGGATACAAA	960
GACTGGATCC TGTGGATTTT CTTTGCCATA TCATGCTTTT TGCTTTGTGT TGTTTTGCTG	1020
GGGTTTCATCA TGTGGGCCTG CCAGAGAGGC AACATTAGGT GCAACATTTG CATTTGAGTG	1080
TATTAGTAAT TAAAAACACC CTTGTTTCTG	1110

SEQ ID NO:58

LENGTH: 346

TYPE:amino acid

STRANDEDNESS:single

TOPOLOGY:linear

MOLECULE TYPE:peptide

SEQUENCE DESCRIPTION:SEQ ID NO:58:

Met Lys Thr Ile Ile Ala Leu Ser Tyr Ile Phe Cys Leu Ala Leu  
-15 -10 -5  
Gly Gln Asp Leu Pro Gly Asn Asp Asn Ser Thr Ala Thr Leu Cys  
1 5 10  
Leu Gly His His Ala Val Pro Asn Gly Thr Leu Val Lys Thr Ile  
15 20 25  
Thr Asp Asp Gln Ile Glu Val Thr Asn Ala Thr Glu Leu Val Gln  
30 35 40  
Ser Ser Ser Thr Gly Lys Ile Cys Asn Asn Ile Asp Thr Cys Ile  
45 50 55  
Ser Glu Cys Ile Thr Pro Asn Gly Ser Ile Pro Asn Asp Lys Pro  
60 65 70  
Phe Gln Asn Val Asn Lys Ile Thr Tyr Gly Ala Cys Pro Lys Tyr  
75 80 85  
Val Lys Gln Asn Thr Leu Lys Leu Ala Thr Gly Met Arg Asn Val  
90 95 100  
Pro Glu Lys Gln Thr Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe  
105 110 115  
Ile Glu Asn Gly Trp Glu Gly Met Ile Asp Gly Trp Tyr Gly Phe  
120 125 130  
Arg His Gln Asn Ser Glu Gly Thr Gly Gln Ala Ala Asp Leu Lys  
135 140 145  
Ser Thr Gln Ala Ala Ile Asp Gln Ile Asn Gly Lys Leu Asn Arg  
150 155 160  
Val Ile Glu Lys Thr Asn Glu Lys Phe His Gln Ile Glu Lys Glu  
165 170 175  
Phe Ser Glu Val Glu Gly Arg Ile Gln Asp Leu Glu Lys Tyr Val  
180 185 190

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Glu Asp Thr Lys Ile Asp Leu Trp Ser Tyr Asn Ala Glu Leu Leu  
195 200 205  
Val Ala Leu Glu Asn Gln His Thr Ile Asp Leu Thr Asp Ser Glu  
210 215 220  
Met Asn Lys Leu Phe Glu Lys Thr Arg Arg Gln Leu Arg Glu Asn  
225 230 235  
Ala Glu Glu Met Gly Asn Gly Cys Phe Lys Ile Tyr His Lys Cys  
240 245 250  
Asp Asn Ala Cys Ile Glu Ser Ile Arg Asn Gly Thr Tyr Asp His  
255 260 265  
Asp Val Tyr Arg Asp Glu Ala Leu Asn Asn Arg Phe Gln Ile Lys  
270 275 280  
Gly Val Glu Leu Lys Ser Gly Tyr Lys Asp Trp Ile Leu Trp Ile  
285 290 295  
Ser Phe Ala Ile Ser Cys Phe Leu Leu Cys Val Val Leu Leu Gly  
300 305 310  
Phe Ile Met Trp Ala Cys Gln Arg Gly Asn Ile Arg Cys Asn Ile  
315 320 325  
Cys Ile  
330